

celine (from cDNA) YEIAPVFLMEQITLKKREIVGMSKDGIFSPGALSNMYSIMARVKFFPEVKTIG

rat (from peptide) YEIAPVFLLEYV-----REIGMPGGS-DGIFSPGALSN-YAMLIARYKHFPEVKEKG




FIGURE 1

Gap Weight: 3.000 Average Match: 0.540
Length Weight: 0.100 Average Mismatch: -0.396

Quality: 856.2 Length: 585
Ratio: 1.464 Gaps: 0

Percent Similarity: 97.436 Percent Identity: 96.068

4817.Pep x Hgt2.Pep

August 22, 1990 08:20 ..

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1  MASPGSGFWSFGSEDGSGDPENPGTARAWCQVAQKFTGGIGNKLCALLYG 50
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51  DSEKPAESGGSVTSRAATRKVACTCDQKPCSCPKGDVNYALLHATDLLPA 100
51  DAEKPAESGGSQPPRAAARKAACACDQKPCSCSKVDVNYAFLHATDLLPA 100
101 CEGERPTLAFLQDVMNILLQYVVKSFDRSTKVIDFHYPNELLQEYNWELA 150
101 CDGERPTLAFLQDVMNILLQYVVKSFDRSTKVIDFHYPNELLQEYNWELA 150
151 DQPQNLEEILTHCQTTTKYAIAKTGHPRYFNQLSTGLDMVGLAADWLTSTA 200
151 DQPQNLEEILMHCQTTTKYAIAKTGHPRYFNQLSTGLDMVGLAADWLTSTA 200
201 NTNMFITYEIAFVFVLLLEYVTLKQMREIIGWPGGSGDGIFSPGGAISNMYA 250
201 NTNMFITYEIAFVFVLLLEYVTLKQMREIIGWPGGSGDGIFSPGGAISNMYA 250
251 MLIARYKMFPEVKEKGMAAVPRLIAFTSEHSHFSLKKGAAALGIGTDSVI 300
251 MMIA RFKMFPEVKEKGMAALPRLIAFTSEHSHFSLKKGAAALGIGTDSVI 300
301 LIKCDERGMIPSDLERRILEVKQKGFVPFLVSATAGTTVYGAFDPLLAV 350
301 LIKCDERGMIPSDLERRILEAKQKGFVPFLVSATAGTTVYGAFDPLLAV 350
351 ADICKKYKIWMHVDAAWGGGLLMSRKHKWKLSGVERANSVTWNPHKMMGV 400
351 ADICKKYKIWMHVDAAWGGGLLMSRKHKWKLSGVERANSVTWNPHKMMGV 400
401 PLQCSALLVREEGLMQSCNQMHASYLFQQDKHYDLSYDTGDKALQCGRHV 450
401 PLQCSALLVREEGLMQNCNQMHASYLFQQDKHYDLSYDTGDKALQCGRHV 450
451 DVFKLWLMWRAKGTGFEAHIDKCLELAELYLYNIIKNREGYEMVFDGKPO 500
451 DVFKLWLMWRAKGTGFEAHVDKCLELAELYLYNIIKNREGYEMVFDGKPO 500
501 HTNVCFWFVPPSLRVLEDNEERMSRLSKVAPVIKARMEYGTTMVSYQPL 550
501 HTNVCFWYIPPSLRTLEDNEERMSRLSKVAPVIKARMEYGTTMVSYQPL 550
551 GDKVNFFRMVISNPAATHQDIDFLIEEIERLGQDL 585
551 GDKVNFFRMVISNPAATHQDIDFLIEEIERLGQDL 585

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FIGURE 4

1 2

3 4

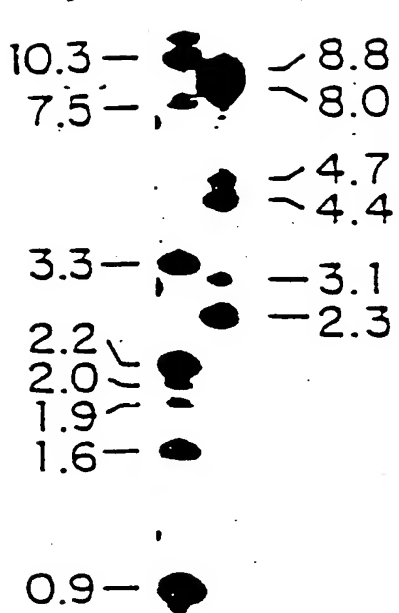


FIGURE 6

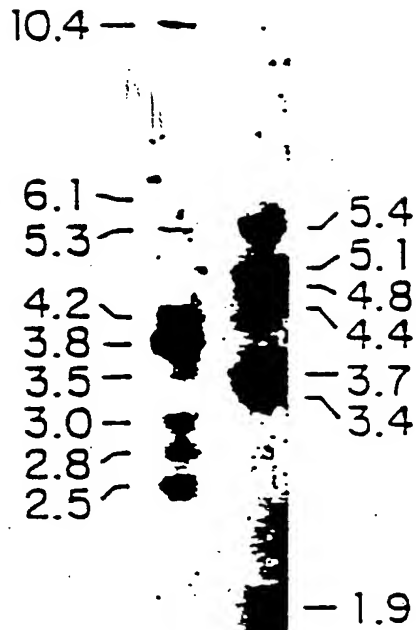


FIGURE 5

3.7 -

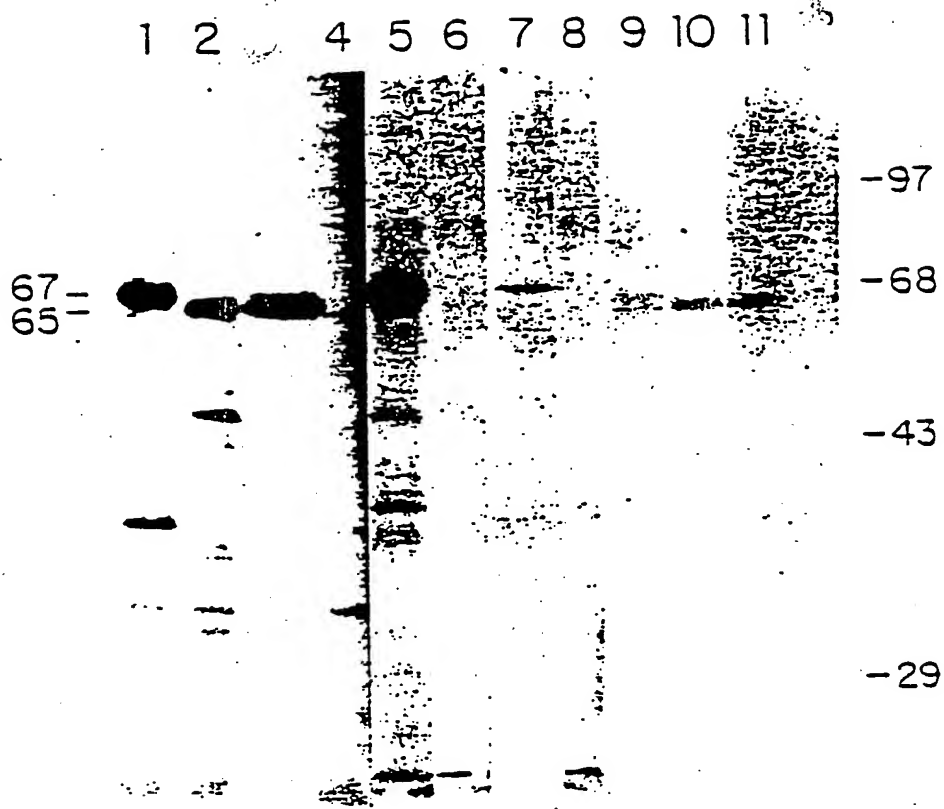


FIGURE 7